

Delaval, Jan

700356

**From:** Roark, Jessica  
**Sent:** Monday, July 01, 2002 4:36 PM  
**To:** Delaval, Jan  
**Subject:** 09/509,283

Jan,

Please search all files for the following from 09/509,283

SEQ ID NO:2.

Results on paper please.

Thanks!

*paper remarks*

*Jessica H. Roark*

CM1 9D04  
Mailbox 9E12  
Art Unit 1644  
703 605-1209

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
jan.delaval@uspto.gov

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## OM protein - protein search, using sw model

Run on: July 1, 2002, 16:45:07 ; Search time 29.77 Seconds

(without alignments)  
742,482 Million cell updates/sec

Title: US-09-509-283b-2

Perfect score: 1082  
Sequence: 1 MMSGWYFPLFLRLRVNG.....YMPRAVNTAKSRDLDTVL 199Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 747574 seqs, 111073796 residues

[ ] number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	19	AAW75956
2	1082	100.0	199	19	AAW75957
3	1082	100.0	199	20	AAV08026
4	1082	100.0	199	21	AAH08731
5	1082	100.0	199	22	AAE03428
6	1082	100.0	199	22	AAE03460
7	1082	100.0	199	22	AAE03525
8	1066.5	98.6	200	21	AAV92213
9	737.5	68.2	200	21	AAH92212
10	734	67.8	200	21	AAH08723
11	722.5	66.8	200	19	AAW75958

12	701	64.8	200	19	AAW71874	Rat cell surface p
13	696	64.3	216	19	AAW71875	Rat cell surface p
14	658	60.8	379	22	AAH67716	Amino acid sequenc
15	449.5	41.5	380	22	AAH67717	Amino acid sequenc
16	146.5	13.5	225	20	AAV41136	Rat CD28 protein s
17	145.5	13.4	221	21	AAV32286	Feline CD28, Fell
18	145.5	13.4	221	21	AAV32279	Cat CD28 receptor.
19	139.5	12.9	220	13	AAH20805	Human CD28 antigen
20	139.5	12.9	220	13	AAH20805	Sequence encoded b
21	139.5	12.9	220	17	AAH02131	Human CD28 cdna pr
22	139.5	12.9	220	17	AAH02131	Human CD28 antigen
23	139.5	12.9	220	18	AAH38413	CD28. Homo sapien
24	138.5	12.9	220	19	AAH80442	Human CD28 antigen
25	139.5	12.9	220	20	AAH8451	Human CD28 antigen
26	139.5	12.9	220	21	AAV96128	Human cell surface
27	139.5	12.9	220	21	AAV44294	Human CD28 recepto
28	139.5	12.9	220	22	AAU02437	Human lymphocyte c
29	134	12.4	225	20	AAV41135	Mouse CD28 protein
30	126	11.6	223	20	AAV41137	Human CD28 protein
31	120.5	11.1	367	18	AAH35862	Human CD28:19G2a c
32	119.5	11.0	134	18	AAH35846	Human CD28 for use
33	119.5	11.0	152	16	AAH67706	CD28 extracellular
34	89.5	8.3	117	20	AAV24469	Human CD28 gene pr
35	89	8.2	305	22	AAH66371	Human partial olfa
36	89	8.2	319	22	AAH71916	Human olfactory re
37	89	8.2	321	22	AAH46999	Human OLFYX protel
38	87.5	8.1	213	22	AAH04561	Human G-protein co
39	87	8.0	223	8	AAV70445	Sequence of mouse
40	86	7.9	223	18	AAH25111	Soluble human CTLA
41	86	7.9	223	22	AAH66519	Human CTLA4. Homo
42	86	7.9	223	22	AAU00687	Human CTLA4 protel
43	85.5	7.9	187	19	AAW29728	Soluble CTLA4 muta
44	84.5	7.8	209	21	AAV94998	Human secreted pro
45	84	7.8	223	21	AAV15129	Human CTLA-4 prote

## ALIGNMENTS

RESULT	1	
AAW75956	AAW75956 standard; Protein: 199 AA.	
XX	AAW75956;	
AC		
XX		
DT	11-DEC-1998 (first entry)	
XX		
DE	Human cell surface protein #1.	
XX		
KW	Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;	
KW	signal transmissiion; autoimmune disorder; allergy; diagnosis;	
KW	mitogen-stimulated.	
XX		
OS	Homo sapiens.	
XX		
PN	W09838216-A1.	
XX		
PD	03-SEP-1998.	
XX		
PF	27-FEB-1998; 98WO-JP00837.	
XX		
PR	26-FEB-1998; 98JP-0062217.	
XX	27-FEB-1997; 97JP-0062290.	
PA	(NLSB ) JAPAN TOBACCO INC.	
XX		
PI	Tamatani T, Tezuka K;	
XX		
DR	WPI: 1998-481144/41.	
XX	N-PSDB; AAV53198.	
PT	Cell surface molecule expressed in thymocytes and lymphocytes and -	
PT	mediating signal transmissiion and cell adhesion, and antibodies to	

PT it useful in treatment of autoimmune and allergic disorders.  
XX  
PS Claim 2; Page 99-101; 149pp; Japanese.  
XX  
CC The present sequence represents a human cell surface protein which is  
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
CC antibodies recognising the cell surface protein. These antibodies also  
CC produce an increase in peripheral blood lymphocytes in the presence of  
CC an antibody recognising CD3 antigen. The cell surface protein contains  
CC the amino acid sequence PDPPF in its extracellular region and the  
CC sequence YMFN in its intracellular region. The cell surface protein can  
CC be used in the prevention and treatment of autoimmune and allergic  
CC diseases, and in the diagnosis and investigation of such disorders.  
XX  
SQ Sequence 199 AA;  
  
Query Match 100.0%; Score 1082; DB 19; Length 199;  
Best Local Similarity 100.0%; Pred. No. 6.6e-116;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKSLWYFELCLRIKVTGTGEINSGANEMFIHNGVQILCKYPDIVQOFKMLKGGQ 60  
Db 1 mkslwyfllclrlkvtlgtgeinsanyemfihngvqilckypdivqikmqllk99q 60  
  
QY 61 ILCDLTKRSGNTVSIKSLKFCCHSOLSNNSVFELYMLDHSNANYFCNLSIFDPPEFK 120  
Db 61 llcdltkrsgntsvsikslkfcchsolnsnsvfelymldhsnanyfcnlsidpppfk 120  
  
QY 121 VTLGGYHIIYESQLCCQKFWLPICGAFVVCILGICILCWLTKKRYSSVHDPNGEY 180  
Db 121 vtlggyhiiyesqlccqkfwlpigcaafvvcilgicilcwltkkryssvndpney 180  
  
QY 181 MEMRAVNTAKKSRLLDVTL 199  
Db 181 mfmraavntakksrlltdvtl 199  
  
RESULT 2  
AAW75957  
ID AAW75957 standard; Protein: 199 AA.  
XX  
AC AAW75957;  
XX  
DT 11-DEC-1998 (first entry)  
XX  
KW Human cell surface protein #2.  
XX  
OS Homo sapiens.  
XX  
PN WO9838216-A1.  
XX  
PD 03-SEP-1998.  
XX  
PE 27-FEB-1998; 98WO-JP00837.  
XX  
PR 26-FEB-1998; 98JP-0062217.  
PR 27-FEB-1997; 97JP-0062290.  
XX  
PA (NISB ) JAPAN TOBACCO INC.  
XX  
PI Tamatani T, Tezuka K;  
XX  
DR WPI; 1998-481144/41.  
XX  
N-PSDB; AAV31199.  
XX  
PT Cell surface molecule expressed in thymocytes and lymphocytes and -  
PT mediating signal transmission and cell adhesion, and antibodies to

PT it useful in treatment of autoimmune and allergic disorders.  
XX  
PS Claim 9; Page 101-105; 149pp; Japanese.  
XX  
CC The present sequence represents a human cell surface protein which is  
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
CC antibodies recognising the cell surface protein. These antibodies also  
CC produce an increase in peripheral blood lymphocytes in the presence of  
CC an antibody recognising CD3 antigen. The cell surface protein contains  
CC the amino acid sequence PDPPF in its extracellular region and the  
CC sequence YMFN in its intracellular region. The cell surface protein can  
CC be used in the prevention and treatment of autoimmune and allergic  
CC diseases, and in the diagnosis and investigation of such disorders.  
XX  
SQ Sequence 199 AA;  
  
Query Match 100.0%; Score 1082; DB 19; Length 199;  
Best Local Similarity 100.0%; Pred. No. 6.6e-116;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MKSLWYFELCLRIKVTGTGEINSGANEMFIHNGVQILCKYPDIVQOFKMLKGGQ 60  
Db 1 mkslwyfllclrlkvtlgtgeinsanyemfihngvqilckypdivqikmqllk99q 60  
  
QY 61 ILCDLTKRSGNTVSIKSLKFCCHSOLSNNSVFELYMLDHSNANYFCNLSIFDPPEFK 120  
Db 61 llcdltkrsgntsvsikslkfcchsolnsnsvfelymldhsnanyfcnlsidpppfk 120  
  
QY 121 VTLGGYHIIYESQLCCQKFWLPICGAFVVCILGICILCWLTKKRYSSVHDPNGEY 180  
Db 121 vtlggyhiiyesqlccqkfwlpigcaafvvcilgicilcwltkkryssvndpney 180  
  
QY 181 MEMRAVNTAKKSRLLDVTL 199  
Db 181 mfmraavntakksrlltdvtl 199  
  
RESULT 3  
AA08026  
ID AA08026 standard; Protein: 199 AA.  
XX  
AC AA08026;  
XX  
DT 08-JUL-1999 (first entry)  
XX  
DE Human activated T-lymphocyte protein 8F4.  
XX  
KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;  
KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;  
KW T cell activation; cytokine synthesis; regulatory element; B cell;  
KW T cell-dependent antibody production; treatment; prevention; cancer;  
KW autoimmune disease; transplant rejection; immune system regulation;  
KW disorder; acquired immune deficiency syndrome; AIDS; asthma.  
XX  
OS Homo sapiens.  
XX  
PN WO9915553-A2.  
XX  
PD 01-APR-1999.  
XX  
PE 23-SEP-1998; 98WO-DE02896.  
XX  
PR 11-MAY-1998; 98DE-1021060.  
PR 23-SEP-1997; 97DE-1041929.  
XX  
PA (DEKO-) DEUT KOCH INST ROBERT.  
PA (BUND ) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.  
XX  
PI Kroczeck R;  
XX  
DR WPI; 1999-276975/23.

DR N-PSDB; AAX37661.  
XX Polypeptide 8F4 co-stimulates T cells and is present only on  
PT activated cells  
XX  
PS Claim 2; Page 24; 47pp; German.  
XX This invention describes a novel human protein, 8F4, and its encoding  
CC nucleic acid which co-stimulates T cells and is present on activated CD4+  
CC and CD8+ T cells but not on resting or activated B cells, granulocytes,  
CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,  
CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a  
CC strong co-stimulatory signal for T cell activation, i.e. it amplifies  
CC proliferation of T cells, synthesis of certain cytokines and other  
CC regulatory agents, and improves T cell-dependent antibody production  
CC by B cells. Agents that inhibit 8F4 are used to treat or prevent  
CC autoimmune diseases, to prevent transplant rejection and to treat  
CC disorders of immune system regulation. 8F4, or cells that express it,  
CC is/are used to treat or prevent cancers, acquired immune deficiency  
CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).  
Sequence 199 AA:  
Query Match 100.0%; Score 1082; DB 20; Length 199;  
Best Local Similarity 100.0%; Pred. No. 6.6e-116;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKSGIWFELFLCRLKRVLTGTEINGSANEMFLFHNGVQIICKYDPDIYOQRFMOLKGGQ 60  
Db 1 mksq1wfyfllcrlkvtlgtelngsanemflfhngvqilckypdiyqkfmgqllksgq 60  
QY 61 ILCDLTKTKGSGNTVSIKSLKFCCHSOLSNNSVSFFLYMJDHSHANYFCNLSIFDPPPFK 120  
Db 61 ilcdltkktgsgntvskslkfcchsqslsnsvsfflyldhshanyfcnlsifdppfk 120  
QY 121 VTLGGYHIIYESQCLCOLKFWLPIGCAFYVVCILGCLILCWLTKKRYSSVHPDNGEY 180  
Db 121 vtlggyihlyesqclckfwlpigcaafvvcilgclilcwltkkryssvhpndgey 180  
QY 181 MEMRAVNTAKKSRLLDVTL 199  
Db 181 mfmraavnlaakksrlltdvcl 199  
RESULT 4  
ID AAB08731 standard; Protein: 199 AA.  
X AAB08731:  
XX 02-JAN-2001 (first entry)  
DT Amino acid sequence of a human CRP1 polypeptide.  
XX  
DE  
KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;  
KW T-lymphocyte activation; type I transmembrane protein; T cell activation;  
KW T cell proliferation; T-cell mediated disorder.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..20  
FT Peptide /note= "signal peptide"  
FT 21..199  
FT Protein /note= "mature protein"  
FT 21..140  
FT Domain /note= "extracellular domain"  
FT 141..161  
FT Domain /note= "predicted transmembrane domain"  
FT 162..199  
FT /note= "intracellular domain"  
XX

PN W0200046240-A2.  
XX 10-AUG-2000.  
XX 27-JAN-2000; 2000WO-US01871.  
XX 03-FEB-1999; 99US-0244448.  
XX 08-MAR-1999; 99US-0264527.  
XX (AMGE-) AMGEN INC.  
XX yoshinaga SK;  
XX WPI; 2000-543476/49.  
DR N-PSDB; AAA64558.  
PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful  
PT in the treatment, prevention and diagnosis of T cell mediated disorders  
XX  
XX Disclosure; Fig 13A; 174pp; English.  
XX  
XX The present sequence represents a CRP1 (CD28 related protein-1)  
CC polypeptide. The specification also describes a B7RP1 (B7 related  
CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte  
CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are  
CC predicted to be a type I transmembrane protein. The nucleic acids are  
CC useful for regulating T cell activation or proliferation in an animal.  
CC The polypeptides are useful for treating, preventing ameliorating or  
CC diagnosing a T-cell mediated disorder in an animal. They can also be  
CC used to identify test molecules that bind to the polypeptides.  
Sequence 199 AA:  
Query Match 100.0%; Score 1082; DB 21; Length 199;  
Best Local Similarity 100.0%; Pred. No. 6.6e-116;  
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKSGIWFELFLCRLKRVLTGTEINGSANEMFLFHNGVQIICKYDPDIYOQRFMOLKGGQ 60  
Db 1 mksq1wfyfllcrlkvtlgtelngsanemflfhngvqilckypdiyqkfmgqllksgq 60  
QY 61 ILCDLTKTKGSGNTVSIKSLKFCCHSOLSNNSVSFFLYMJDHSHANYFCNLSIFDPPPFK 120  
Db 61 ilcdltkktgsgntvskslkfcchsqslsnsvsfflyldhshanyfcnlsifdppfk 120  
QY 121 VTLGGYHIIYESQCLCOLKFWLPIGCAFYVVCILGCLILCWLTKKRYSSVHPDNGEY 180  
Db 121 vtlggyihlyesqclckfwlpigcaafvvcilgclilcwltkkryssvhpndgey 180  
QY 181 MEMRAVNTAKKSRLLDVTL 199  
Db 181 mfmraavnlaakksrlltdvcl 199  
RESULT 5  
ID AAE03428 standard; Protein: 199 AA.  
X AAE03428:  
XX 10-AUG-2001 (first entry)  
DT Human gene 2 encoded secreted protein HT2SG64, SEQ ID NO: 111.  
XX  
XX Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
KW foetal abnormality; developmental abnormality; hematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
KW angiotensin disorder; kidney disorder; gastrointestinal disorder; allergy;  
KW

KW pregnancy-related disorder; endocrine disorder; infection; wound healing;  
KM cell culture; chemotaxis; vunerary; binding partner identification;  
XX gene therapy.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein 20..111  
FT /note= "Mature human secreted protein"  
XX  
PN WO200132675-A1.  
XX  
PD 10-MAY-2001.  
XX  
PE 25-OCT-2000; 2000WO-US29363.  
XX  
PF 29-OCT-1999; 99US-0162239.  
XX  
PR 30-JUN-2000; 2000US-0215139.  
XX  
PI (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;  
DR WPI; 2001-328772/34.  
DR N-PSDB; AAD07810.  
XX  
PT Thiry two human secreted proteins, useful for treating cancers,  
PT hyperproliferative disorders, inflammatory disorders, neurological  
PT disorders, autoimmune diseases and cardiovascular disorders -  
XX  
XX Claim 11; Page 471; 576pp; English.  
XX  
CC AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted  
CC protein genes, and AAE03427-AAE03523 represent the proteins they encode.  
CC AAE03524-AAE03537 represent human secreted protein fragments or variants.  
CC The secreted proteins and their genes are useful for preventing, treating  
CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
CC Pathological conditions can be diagnosed by determining the amount of the  
CC new protein in a sample or by determining the presence of mutations in  
CC the new genes. Specific uses are described for each of the 32 genes,  
CC based on the tissues in which they are most highly expressed, and include  
CC developing products for the diagnosis or treatment of proliferative  
CC disorders, cancer, tumours, foetal and developmental abnormalities,  
CC hematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
CC pregnancy-related disorders, endocrine disorders, and infections. The  
CC proteins can also be used to aid wound healing and epithelial cell  
CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
CC before transplantation, for supporting cell culture of primary tissues,  
CC to regenerate tissues, to identify their cognate ligands or binding  
CC partners, and in chemotaxis, and can be used as a food additive or  
CC preservative to modify storage properties. Antibodies specific for a  
CC protein of the invention can be used in alleviating symptoms associated  
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).  
CC The present sequence represents a human secreted protein of  
CC the invention.  
XX  
SQ Sequence 199 AA;  
XX  
Query Match 100.0%; Score 1082; DB 22; Length 199;  
Best Local Similarity 100.0%; Pred. No. 6, 6e-116;  
Matches, 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MKSLWFFPCLRIKVTGEINGSANWEMIFHNGGVOLICKPDIYQGRKMLKGGQ 60  
|||||

Db 1 mksglwyfficllrklvtgelingsanyemiflmngvgvllckypdlvqgfkmgllkgyg 60  
Qy ILCDLTKRGSGNTVSTKSLKFCHSOLSNNSEFVLNLDHSHANYFCNLSIDPPPFK 120  
61 |||||||  
Db 61 llcdltktksgsgntvstkslkslfcshqslsmnsvsffllynltdshanyfclnsldpppfk 120  
121 VTLTGGLYHLIYESQLCCQLKFWLPDGGCAAFVYVLCILCWLTKRKRSSVHDNGEY 180  
Db 121 vtlcgyylhiyesqlccqlkfwlpdggcaafvvcilgcllclwltkrkyssvhdnpgey 180  
Qy 181 MEMRAVNTAKSRRLTDVTL 199  
181 |||||||  
Db 181 mfmraavnltakskrltdvtl 199  
RESULT 6  
AAE03460  
ID AAE03460 standard; Protein: 199 AA.  
XX  
AC AAE03460;  
XX  
DT 10-AUG-2001 (first entry)  
XX  
DE Human gene 2 encoded secreted protein HT2SG64, SRQ ID NO: 143.  
XX  
KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
KW foetal abnormality; developmental abnormality; hematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;  
KW pregnancy-related disorder; endocrine disorder; infection; wound healing;  
KW cell culture; chemotaxis; vunerary; binding partner identification;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein 20..199  
FT /note= "Mature human secreted protein"  
XX  
XX WO200132675-A1.  
XX  
XX 10-MAY-2001.  
XX  
XX 25-OCT-2000; 2000WO-US29363.  
XX  
XX 29-OCT-1999; 99US-0162239.  
XX  
XX 30-JUN-2000; 2000US-0215139.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;  
DR WPI; 2001-328772/34.  
DR N-PSDB; AAD07842.  
XX  
PT Thiry two human secreted proteins, useful for treating cancers,  
PT hyperproliferative disorders, inflammatory disorders, neurological  
PT disorders, autoimmune diseases and cardiovascular disorders -  
XX  
XX Claim 11; Page 489-490; 576pp; English.  
XX  
XX AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted  
XX protein genes, and AAE03427-AAE03523 represent the proteins they encode.  
XX AAE03524-AAE03537 represent human secreted protein fragments or variants.  
XX The secreted proteins and their genes are useful for preventing, treating  
XX or ameliorating medical conditions, e.g., by protein or gene therapy.  
XX Pathological conditions can be diagnosed by determining the amount of the  
XX new protein in a sample or by determining the presence of mutations in

the newgenes. Specific uses are described for each of the 32 genes. based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of the invention.

**SQ**      **Sequence**      **199 AA;**

Query Match	100.0%	Score 1082	DB 22	Length 199
Best Local Similarity	100.0%	Pred. No. 6.6e-116		
Matches 199, Conservative	0	Mismatches 0	Indels 0	Gaps 0

QY 1 M K S G L W Y F F L E C L R I K V L T G E I N G S A N Y E M F I F H N G G V Q I L C K Y P D I V Q O F K M O L L K G G C

Db 1 mksqjwyfflfcrlkvlgtelngsanymfifhngvqilckypdvvqfkmqlkgygc

QY 61 ILCDLTKTSGSNTVSIKSLKECHSOLSNSVSFFLYNLDSHANYFCNLSTFDPPFK 120

Db 61 11cdltktgsgntvsi k fchsglsnsvsfflynl dshanyf cnl sif dppfk 120

QY 121 VTLTGGYLHIYESQLCCQLKFWLPIGCAAFVVCILGCLICWLTKKKYSSSVHDPNGEY 180

Db 121 vlttgylhlyesqlccqkfwlprigcaafvvcllgcllcwlttkkkysssvhdngey 180

QY 181 MEMRAVNTAKKSRLTDVTL 199

```
Db 181 mfmravntakksrltdvtl 199
```

RESULT 7  
AAE03525  
AAE03525 standard; Protein; 199 AA

DT 10-AUG-2001 (first entry)

Human secreted protein variant, SEQ ID NO: 211

Human secreted protein variant, SEQ ID NO: 211

KW Human, secreted protein; proliferative disorder; cancer; tumour; asthma  
KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; Rheumatoid arthritis;  
KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
KW parotitis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
KW angiodysplastic disorder; kidney disorder; gastrointestinal disorder; allergy  
KW pregnancy-related disorder; endocrine disorder; infection; wound healing  
KW cell culture; chemotaxis; vulnerability; binding partner identification;  
KW gene therapy.

XX	Homo sapiens
OS	

XX  
DN - W0300133675-21

XX

PD 10-MAY-2001.

XX  
PF 25-OCT-2000; 2000WO-US29363.

PR 29-OCT-1999; 99US-0162239.

PR 30-JUN-2000; 200005-0215139  
XX

PA (HUMA-) HUMAN GENOME SCI INC.  
YY

PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE,

DR WPI; 2001-32872/34

PT Thirty two human secreted proteins, useful for treating cancers, hyperproliferative disorders, inflammatory disorders, neurological disorders, autoimmune diseases and cardiovascular disorders -

PS Disclosure; page 524; 576pp; English.

CC AAD07680-907 represent cDNA corresponding to 32 human secreted  
CC proteins and, and AAD03427-AAE03523 represent the proteins they encode.  
CC AAE03524-AAE03537 represent human secreted protein fragments or variants.  
CC The secreted proteins and their genes are useful for preventing, treating  
CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
CC Pathological conditions can be diagnosed by determining the amount of the  
CC new protein in a sample or by determining the presence of mutations in  
CC the new genes. Specific uses are described for each of the 32 genes,  
CC based on the tissues in which they are most highly expressed, and include  
CC developing products for the diagnosis or treatment of proliferative  
CC disorders, cancer, tumours, foetal and developmental abnormalities,  
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
CC angiotensin disorders, kidney disorders, gastrointestinal disorders,  
CC pregnancy-related disorders, endocrine disorders, and infections. The  
CC proteins can also be used to aid wound healing and epithelial cell  
CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
CC before transplantation, for supporting cell culture of primary tissues,  
CC to regenerate tissues, to identify their cognate ligands or binding  
CC partners, and in chemotaxis, and can be used as a food additive or  
CC preservative to modify storage properties. Antibodies specific for a  
CC protein of the invention can be used in alleviating symptoms associated  
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).  
CC The present sequence represents a human secreted protein variant  
CC referred to in the disclosure of the invention.

SQ Sequence 199 AA

Query Match	100.0%	Score 1082;	DB 22;	Length 199;
Best Local Similarity	100.0%;	Pred. No. 6;	6e-11;	
Matches 199; Conservative	0;	Mismatches	0;	Gaps 0;

QY 1 M K S G L W F F L F C L R I K V L T G E I N S A N Y E M F I F H N G V Q I L C K Y P D I V Q Q F K M O L L K G G Q

Db 1 mksglwyfflfcrlkvlgtginsanyemfifhngvgqlckypdivqfkmqlkggg

QY 61 ILCDLTKTGSGNTVSIKSLKFCHSOLSNSVSFFLYNLDHSHANYFCNLSIFDPPFK 120

Db 61 11cd1tktgsgntvsiks1kfchsgqlsnsvsfflynlhdshanyfclnls1fdpppfk 120

QY 121 VTLTGGLHIYESQLCCQLKFWLPIGCAAEVVCILGCILCWLTKKKYSSSVHDPNGEY 180

Db 121 vtltgylhiyesqlccqlkfwlpigcaafvvvcilqlcillcwltkkkysssvhdpnqey 180

QY 181 MEMRAVNTAKKSRLTDVTL 199

Db 181 mfmravntakksrjtdvtl 199

## RESULT 8

ID	AAV92213
AC	AAV92213 standard; Protein: 198 AA.
XX	
XX	AAV92213;
DT	10-AUG-2000 (first entry)
DE	Human Th2-specific polypeptide, h1228.
KW	h1228; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
KM	CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
KW	antipruritic; antiallergic; antiallergic; anti-viral; ophthalmologic;
KM	CTLA-4; nephrotropic; anti-HIV; antibacterial.
XX	
OS	Homo sapiens.
XX	
FH	
FT	Key Location/Qualifiers
FT	Peptide 113..318
FT	/label= conserved_PPP_motif
FT	/note= "common in CD28 and CTLA-4"
FT	178..181
FT	/label= YXXM motif
FT	/note= "common in CD28 and CTLA-4; necessary for
FT	CD28-mediated phosphatidylinositol 3-kinase
FT	activity"
PN	WO200019988-A1.
XX	
PD	13-APR-2000.
XX	
PF	06-OCT-1999; 99WO-US23156.
PR	07-OCT-1998; 98US-0168229.
PR	26-FEB-1999; 99US-0258670.
PR	06-OCT-1999; 99US-0413136.
PA	(MILL-) MILLENNIUM PHARM INC.
PX	
PI	Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
DR	WPI: 2000-303619/26.
N-PSDB:	AAA09056.
PT	T helper (Th) 2 nucleic acids and encoded proteins, useful for the
PT	diagnosis and treatment of immune and respiratory disorders such as
PT	Crohn's diseases, arthritis, insulin dependent diabetes and
PT	autoimmunity
CL	Claim 16; Page 138-139; 159pp; English.
CC	This Th2-specific polypeptide, which has similarity to human CD28 and
CC	human CTLA-4 is encoded by human orthologue h1228.
CC	A novel method for modulating a Th2 response, an immune response, or
CC	suppressing airway inflammation or hyperresponsiveness in a mammal
CC	comprises administering a Th2-specific polypeptide of the invention, an
CC	antibody to such a polypeptide or allelic variants of the genes. The
CC	novel DNA and polypeptide sequences are useful for treatment and
CC	diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases
CC	arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
CC	dermatitis, psoriasis, graft rejection, graft versus host diseases,
CC	sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
CC	viral infections (including human immunodeficiency virus (HIV)),
CC	bacterial infections, bronchitis, cystic fibrosis, diptheria,
CC	emphysema, pneumonia, and Legionnaires disease.
SO	Sequence 198 AA;
Query Match	98.6%; Score 1066.5; DB 21; Length 198;
Best Local Similarity	99.5%; Pred. No. 3.9e-114;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1	
1 MKSGILWFELCLRIRKVLGTGEINSANYEMFIFNGVGVIATCRYPDIIYVOFKMKQLKGGO 60	

Db	1	msksglywifeflclolrkivlgeingnsanyemifhngvgvllckypdlvqgfkmpqlkkgqg	60
Qy	61	IIICDLTKRTSGSGWTVSIRKSLFCHSOLSNNNSVFFLYNLDHSHANYFCNLSTFDPPPK	120
Db	61	IIICDLTKRTSGSNVTSIKSLFCHSGLSNNNSVFFLYNLDHSHANYFCNLSTFDPPPK	120
Qy	121	VTLTGGLHIYVSQLOCCQKLFMLPTICAAFWVVCILGICILICMLTKRKYSVHDPNGEY	180
Db	121	VLTGGLYHLYVSQLOCCQKLFwlpigcaafvvcilgicilicmltckkysvvhdpngey	179
Qy	181	MEMRAVNTAKKSHLDVTL	199
Db	180	mfmravnlakksrltdvtl	198
RESULT 9			
AAV92212			
ID	AAV92212	standard; Protein; 200 AA.	
XX	AAV92212;		
DT	10-AUG-2000	(first entry)	
DE	Murine Th2-specific polypeptide, m1228.		
XX	m1228: Th2-specific; T helper cell; anti-inflammatory; antiarthritic;		
KW	CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;		
KM	antiproliferic; antitachycardic; antiallergic; anti-viral; optalmalologica		
KW	CTLA-4; nephrotropic; anti-HIV; antibacterial.		
OS	Mus musculus.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	114..119	
FT		/Label= conserved_PPP_motif	
FT		/note= "common in CD28 and CTLA-4"	
FT	Peptide	181..184	
FT		/Label= YXXM_motif	
FT		/note= "common in CD28 and CTLA-4; necessary for	
FT		CD28-mediated phosphatidylinositol 3-kinase	
FT		activity"	
XX			
XX	WO200019988-A1.		
XX	13-APR-2000.		
PD			
XX	06-OCT-1999;	99WO-US23156.	
PF			
XX	07-OCT-1998;	98US-0168229.	
PR	26-FEB-1999;	99US-0258670.	
PR	06-OCT-1999;	99US-0413136.	
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;		
XX			
DR	WPI: 2000-303619/26.		
DR	N-PSDB; AAA09054.		
XX			
PT	T helper (Th) 2 nucleic acids and encoded proteins, useful for the		
PT	diagnosis and treatment of immune and respiratory disorders such as		
PT	Crohn's diseases, arthritis, insulin dependent diabetes and		
PT	autoimmunity		
XX			
PS	Claim 16; Page 130-131; 159pp; English.		
XX			
CC	This Th2-specific polypeptide is encoded by a murine orthologue m1228.		
CC	The protein shares homology with both human and murine CD28 and CTLA-4.		
CC	A novel method for modulating a Th2 response, an immune response, or		
CC	suppressing airway inflammation or hypersensitivity in a mammal		
CC	comprises administering a Th2-specific polypeptide of the invention, an		
CC	antibody to such a polypeptide or allelic variants of the genes. The		





DR WPI; 1998-481144/41.  
DR N-PSDB; AAV53200.  
XX  
XX  
PT Cell surface molecule expressed in thymocytes and lymphocytes and -  
PT mediating signal transmission and cell adhesion, and antibodies to  
PT it useful in treatment of auto-immune and allergic disorders.  
XX  
XX  
PS Claim 9; Page 110-112; 149pp; Japanese.  
XX  
XX  
CC The present sequence represents a mouse cell surface protein which is  
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
CC antibodies recognising the cell surface protein. These antibodies also  
CC produce an increase in peripheral blood lymphocytes in the presence of  
CC an antibody recognising CD3 antigen. The cell surface protein contains  
CC the amino acid sequence FDPPEF in its extracellular region and the  
CC sequence YMFH in its intracellular region. The cell surface protein can  
CC be used in the prevention and treatment of autoimmune and allergic  
CC diseases, and in the diagnosis and investigation of such disorders.  
Sequence 200 AA;

Query Match 66.8%; Score 722.5; DB 19; Length 200;  
Best Local Similarity 68.3%; Pred. No. 1.2e-74;  
Matches 136; Conservative 20; Mismatches 42; Indels 1; Gaps 1;

QY 1 MKSLMWFLEFLRKYLTGEINGSANVEMFIFHNGGVQILCKYDPIVOQFMQLKGGQ 60  
DB 1 mkpfcvfvfcflrlitgelsadhrmfngvqskypcvqklmrlfere 60  
QY 61 ILCLDITKSGNTVSIRKSLKFSQSLSNNSVSFFLYNLDSHANYFCNLSTFDPPPK 120  
DB 61 vlclctktkggnavsklmpclclhlsnsvsfflmpdsqsgyfcslftdppfq 120  
QY 121 V-TTGGVLIHYESQLCCQKLFMLPGCAAFVYVCIIGCLICLTKKKYSSVHPDNGE 179  
DB 121 ernlsgyylhyesqlcqlklwlpvglpalrvvlltgcillwfskkyssvhdnpse 180  
QY 180 YMFHRAVNTAKKSRRLDVT 198  
DB 181 ymfmaavntkksrslagvt 199

RESULT 12  
AAW71874  
ID AAW71874 standard; Protein; 200 AA.  
XX  
XX AAW71874;

DT 11-DEC-1998 (first entry)  
DE Rat cell surface protein #1.  
XX  
XX Rat; cell surface protein; thymocyte; lymphocyte; cell adhesion;  
KW signal transmission; autoimmune disorder; allergy; diagnosis;  
KW mitogen-stimulated.  
XX  
XX Rattus sp.  
OS  
XX  
XX WO9838216-A1.  
PN  
XX  
PD 03-SEP-1998.  
XX  
XX 27-FEB-1998; 98WO-JP00837.  
PF  
XX  
XX 26-FEB-1998; 98JP-0062217.  
PR 27-FEB-1997; 97JP-0062290.  
XX  
XX (NISR ) JAPAN TOBACCO INC.  
PA  
XX  
XX Tamatahi T, Tezuka K;  
PI  
XX

DR WPI; 1998-481144/41.  
DR N-PSDB; AAV61357.  
XX  
XX  
PT Cell surface molecule expressed in thymocytes and lymphocytes and -  
PT mediating signal transmission and cell adhesion, and antibodies to  
PT it useful in treatment of auto-immune and allergic disorders.  
XX  
XX  
PS Claim 9; Page 106-109; 149pp; Japanese.  
XX  
XX  
CC The present sequence represents a rat cell surface protein which is  
CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
CC antibodies recognising the cell surface protein. These antibodies also  
CC produce an increase in peripheral blood lymphocytes in the presence of  
CC an antibody recognising CD3 antigen. The cell surface protein contains  
CC the amino acid sequence FDPPEF in its extracellular region and the  
CC sequence YMFH in its intracellular region. The cell surface protein can  
CC be used in the prevention and treatment of autoimmune and allergic  
CC diseases, and in the diagnosis and investigation of such disorders.  
Sequence 200 AA;

Query Match 64.8%; Score 701; DB 19; Length 200;  
Best Local Similarity 67.9%; Pred. No. 3.7e-72;  
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

QY 7 YF--FLECLRIKYLTEINGSANVEMFIFHNGGVQILCKYDPIVOQFMQLKGGQILC 63  
DB 4 yfscvfvfcflrlitgelnahrmfshdgvqskypcvqklmrlfdreylc 63  
QY 64 DLTKKSGNTVSIRKSLKFSQSLSNNSVSFFLYNLDSHANYFCNLSTFDPPPK-KVT 122  
DB 64 dltkksgntvsklmpmscopyqlsnsvsffldnadsgsyfclslftdppfgekn 123  
QY 123 LTGGVLIHYESQLCCQKLFMLPGCAAFVYVCIIGCLICLTKKKYSSVHPDNGEYMF 182  
DB 124 lsgyylhyesqlcqlklwlpvgcaafvaalltgcilwfskkyssvhdnpseymf 183  
QY 183 MRAVNTAKKSRRLDVT 198  
DB 184 maavntkksrslagmt 199

RESULT 13  
AAW71875  
ID AAW71875 standard; Protein; 216 AA.  
XX  
XX AAW71875;

DT 11-DEC-1998 (first entry)  
DE Rat cell surface protein #2.  
XX  
XX Rat; cell surface protein; thymocyte; lymphocyte; cell adhesion;  
KW signal transmission; autoimmune disorder; allergy; diagnosis;  
KW mitogen-stimulated.  
XX  
XX Rattus sp.  
OS  
XX  
XX WO9838216-A1.  
PN  
XX  
PD 03-SEP-1998.  
XX  
XX 27-FEB-1998; 98WO-JP00837.  
PF  
XX  
XX 26-FEB-1998; 98JP-0062217.  
PR 27-FEB-1997; 97JP-0062290.  
XX  
XX (NISR ) JAPAN TOBACCO INC.  
PA  
XX  
XX Tamatani T, Tezuka K;  
PI  
XX

DR WPI: 1998-481144/41.  
 DR -PSSB; AAV61358.  
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -  
 PT mediating signal transmission and cell adhesion, and antibodies to  
 PT it useful in treatment of auto-immune and allergic disorders.  
 PS  
 PS Claim 9; Page 112-115; 149pp; Japanese.  
 XX  
 CC The present sequence represents a rat cell surface protein which is  
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell  
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to  
 CC antibodies recognising the cell surface protein. These antibodies also  
 CC produce an increase in peripheral blood lymphocytes in the presence of  
 CC an antibody recognising CD3 antigen. The cell surface protein contains  
 CC the amino acid sequence FDDPPF in its extracellular region and the  
 CC sequence YMFV in its intracellular region. The cell surface protein can  
 CC be used in the prevention and treatment of autoimmune and allergic  
 CC diseases, and in the diagnosis and investigation of such disorders.  
 XX  
 SS Sequence 216 AA;  
 ●  
 Query Match 64.3%; Score 696; DB 19; Length 216;  
 Best Local Similarity 68.8%; Pred. No. 1.5e-71;  
 Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2  
 QY 7 YF---EFLCLRIKVLGTGEINGSANTYEMFIFHNGVOILCKYPDIQOFKMLKGGQILC 63  
 Db 4 Yfcscvfcfcflklilgtlndlanhrmtsfhdgyqgisconyvetvqqlkmqlfkdkrevlc 63  
 QY 64 DLRTKSGGNVYSIKSLKFCFHSQLSNNSVSPFLYMLDHSNARYCNLSIFDPPPF-KVT 122  
 Db 64 dlrtksggnvtslknpmscpyqlsnnsvsflldadssqgsyflcslstfdpppfqkn 123  
 QY 123 LTGGGLIHTYESOLCCQLKFWLPICGAPEVWVCIILCIIILWTKKKRYSSVHDPPGCEYMF 182  
 Db 124 lsgyylilyesqqlccqlklwlpvgcaatfaaalifgcilfwfakkkryssvhdppnseynf 183  
 QY 183 MRAVNTAKKSRL 194  
 Db 184 maavntkkksrl 195  
 RESULT 14  
 AAB67716  
 ID AAB67716 standard; Protein; 379 AA.  
 XX  
 XX AAB67716;  
 ●  
 DE 11-JUN-2001 (first entry)  
 XX  
 XX Amino acid sequence of hICOS-mIgG2m fusion protein.  
 DE  
 XX GL50; antigen; antigen presenting cell; T cell proliferation; tumour;  
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;  
 OS acquired immune deficiency syndrome; AIDS; vaccine.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS Mus musculus.  
 PN WO200121796-A2.  
 XX  
 XX 29-MAR-2001.  
 PD  
 PF 21-SEP-2000; 2000WO-US25892.  
 XX  
 PR 21-SEP-1999; 99US-0155043.  
 XX  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 XX Ling V, Dunussi-Joannopoulos K;

XX WP1: 2001-244938/25.  
 DR N-PSDB; AAF79939.  
 XX  
 PT New isolated nucleic acid encoding a GL50 polypeptide for modulating a  
 XX immune response and reducing the proliferation of a tumour cell -  
 XX  
 PS Disclosure; Fig 26B; 195pp; English.  
 CC  
 CC The present sequence represents a fusion protein, comprising human ICOS  
 CC (hICOS) and murine IgG2a (mIgG2a). The fusion protein is used in the  
 CC course of the invention. The specification describes GL50 polypeptides.  
 CC GL50 molecules are antigens on the surface of antigen presenting cells,  
 CC which costimulate T cell proliferation and bind to costimulatory receptor  
 CC ligands on T cells. GL50 modulating agents are used to modulate an immune  
 CC response in a subject. GL50 polypeptides are used to modulate T cell  
 CC costimulation, and to reduce the proliferation of a tumour cell. Diseases  
 CC that can be treated using GL50 molecules are graft-versus-host disease,  
 CC autoimmune disease, allergies, acquired immune deficiency syndrome  
 CC (AIDS), and viral infections. The GL50 molecules can be used in vaccines.  
 CC GL50 polynucleotides can be used to locate gene regions associated with  
 CC genetic disease, in tissue typing, and in forensic identification of a  
 CC biological sample.  
 CC  
 SQ Sequence 379 AA;  
 XX  
 XX  
 Query Match 60.8%; Score 658; DB 22; Length 379;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-67;  
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 21 EINGSANTYEMFIFNGVQILCKTPDIVQPFKQMLKGGQILCDLTKTKSGNTVSISKSL 80  
 DB 26 eingsantymfifngvqilcktpdivqpfkmgllksgqilcdltkksqntvsisksl 85  
 QY 81 KECHSOISNNVSFEIYNLDHSHANYFCNLTSDPPEFKTLGGYCHAYESQLCOLK 140  
 DB 86 kfchsoisnnsvsfeliynldhshanyfclnltstppfkyltggylhaysqlcqlk 145  
 QY 141 F 141  
 DB 146 f 146  
 RESULT 15  
 AAB67717  
 ID AAB67717 standard; Protein; 380 AA.  
 AC AAB67717;  
 XX  
 DE 11-JUN-2001 (first entry)  
 XX  
 DE Amino acid sequence of mICOS-mIgG2a fusion protein.  
 KW GL50; antigen; antigen presenting cell; T cell proliferation; tumour;  
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;  
 KW acquired immune deficiency syndrome; AIDS; vaccine.  
 XX  
 OS Synthetic.  
 OS Mus musculus.  
 XX  
 MO200121796-A2.  
 XX  
 PD 29-MAR-2001.  
 XX  
 PD 21-SEP-2000; 2000WO-0525892.  
 XX  
 PP 21-SEP-1999; 99US-0155043.  
 XX  
 PA (GENY ) GENETICS INST. INC.  
 XX  
 ILing V, Dunussi-Joannopoulos K;



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OM protein - protein search, using sw model

Run on: July 1, 2002, 16:45:37 ; Search time 19.71 Seconds

(without alignments)  
970.156 Million cell updates/sec

Title: US-09-509-283B-2

Perfect score: 1082

Sequence: 1 MKSGLMYFFFLCRLRIKVLG.....YMFRAVNVAKSRLLDVTLL 199

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 9  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	2	inducible T-cell c
2	701	64.8	200	2	activation-inducib
3	696	64.3	216	2	activation-inducib
4	152	14.0	218	2	T-cell surface gly
5	150.5	13.9	221	2	CD28 precursor - T
6	139.5	12.9	173	2	cell surface prote
7	139.5	12.9	220	1	T-cell surface gly
8	138	12.8	218	2	T-cell surface gly
9	103.5	9.6	218	2	hypothetical prote
10	97	9.0	221	2	CH28 protein - ch
11	91.5	8.5	383	2	hypothetical prote
12	87	8.0	330	2	Fc gamma (IgG) rec
13	87	8.0	330	2	Fc gamma (IgG) rec
14	87	8.0	330	2	Fc gamma (IgG) rec
15	86.5	8.0	330	2	hypothetical prote
16	86	7.9	223	2	cytotoxic T-lympho
17	84	7.8	283	1	cytotoxic T-lympho
18	84	7.8	285	2	Fc gamma (IgG) rec
19	83.5	7.7	186	2	conserved hypother
20	82.5	7.6	248	1	cytotoxic T-lympho
21	81	7.5	276	2	probable glycoprot
22	81	7.5	680	2	31.6k hypothetical
23	81	7.5	1584	2	killer cell inhibi
24	80.5	7.4	247	2	hypothetical prote
25	80.5	7.4	635	2	hypothetical prote
26	78	7.2	231	2	killer cell inhibi
27	77.5	7.2	80	2	hypothetical prote
28	77.5	7.2	220	2	37k proline-rich s
29	77.5	7.2	1070	2	protein-tyrosine k

30	77	7.1	338	2	T34364	hypothetical prote
31	77	7.1	2104	2	D91286	hypothetical prote
32	77	7.1	2104	2	H86127	hypothetical prote
33	76.5	7.1	223	2	I46696	CTLA-4 precursor -
34	76.5	7.1	323	2	S06946	Fc gamma (IgG) rec
35	76.5	7.1	1237	2	A54080	protein-tyrosine-p
36	76	7.0	301	2	I54209	hypothetical prote
37	76	7.0	317	2	J10118	hypothetical prote
38	76	7.0	546	2	S52053	Fc gamma (IgG) rec
39	75.5	7.0	261	2	S29360	cytochrome-c oxida
40	75.5	7.0	277	2	T21330	Fc gamma (IgG) rec
41	75.5	7.0	235	2	T14602	hypothetical prote
42	75	6.9	418	2	AD3417	variant-specific s
43	75	6.9	1132	1	GSBPL	transporter, mts s
44	74.5	6.9	201	2	G90134	host specificity p
45	74.5	6.9	235	2	I50610	hypothetical prote
						T-cell surface gly

## ALIGNMENTS

RESULT	1	
S78540	inducible T-cell co-stimulator ICOS precursor - human	
C:Species: Homo sapiens (man)		
C>Date: 05-Mar-1999 #sequence: revision 05-Mar-1999 #text_change 07-May-1999		
C:Accession: S78540; S78748; S78749		
R:Kroczeck, R.		
submitted to the Protein Sequence Database, June 1998		
A:Reference number: S78540		
A:Accession: S78540		
A:Molecule type: mRNA		
A:Residues: 1-199 <KRO>		
A:Experimental source: cell line MOLT-4V		
R:Hutloff, A.; Dittlich, A.M.; Beier, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop		
Nature 397, 263-266, 1999		
A:Title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela		
A:Reference number: S78748; M01D:99127892		
A:Accession: S78748		
A:Molecule type: mRNA		
A:Residues: 1-199 <HUT1>		
A:Experimental source: cell line MOLT-4V		
A:Accession: S78749		
A:Molecule type: protein		
A:Residues: 'X', 193-198 <HUT2>		
A:Experimental source: cell line MOLT-4V		
C:Complex: homodimer		
C:Superfamily: immunoglobulin homology		
C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein		
F:1-19/Domain: (or 1-20) signal sequence #status predicted <Sig>		
F:20-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <MNT>		
F:21-138/Domain: extracellular #status predicted <EXT>		
F:26-132/Domain: immunoglobulin homology <IMM>		
F:139-164/Domain: transmembrane #status predicted <TM>		
F:165-199/Domain: intracellular #status predicted <INT>		
F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted		
Query Match	100.0%;	Score 1082; DB 2; Length 199;
Best Local Similarity	100.0%;	Pred. No. 3,1e-97;
Matches 199; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MKSGLMYFFFLCRLRIKVLGELNGSANYEMFLFHNGGVQILCKYDPDIYQOFKMLLKGGQ 60
DB	1	MKSGLMYFFFLCRLRIKVLGELNGSANYEMFLFHNGGVQILCKYDPDIYQOFKMLLKGGQ 60
QY	61	ILCDLTKTKGSGNTVSIRKLRCHSOLSNNSVSFFLYNLDHSHANYFCNLSTFPDPPPK 120
DB	61	ILCDLTKTKGSGNTVSIRKLRCHSOLSNNSVSFFLYNLDHSHANYFCNLSTFPDPPPK 120
QY	121	VLTGGLHYTESOLCCOLKFWLPIGCAAFVYVCTIGCTILCMLTKRKSSSVHPNGEX 180
DB	121	VLTGGLHYTESOLCCOLKFWLPIGCAAFVYVCTIGCTILCMLTKRKSSSVHPNGEX 180

OY 181 MEMRAVNTAKKSRLTDVTL 199  
Db 181 MEMRAVNTAKKSRLTDVTL 199

RESULT 2  
activation-inducible lymphocyte immunostimulatory molecule-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 17-Nov-2000

C:Accession: J07397; PC7100

R:Tezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, Blochem. Biophys. Res. Commun. 276, 335-345, 2000

A:Title: Identification and characterization of rat AILIM/ICOS, a novel T-cell costimulatory molecule

A:Contents: Spleen

A:Accession: J07397

A:Residues: 1-200 <TE2>

A:Accession: PC7100

A:Residues: 21-40 <TE2>

C:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.

C:Genetics:

A:Gene: a11m-2

C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 64.8%; Score 701; DB 2; Length 200;  
Best Local Similarity 67.9%; Pred. No. 2.2e-60;  
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2;

OY 7 YF---FLFCLRIKVLTEGINSANVEMFIFHNGVOILCKPDIYQOFKMLKGGQILC 63  
Db 4 YFSCVFVFCFLIKLTGLDLNLRHMFSPHDSGVQISCNPEYQOLKMLFDRVLC 63  
OY 64 DLTKKSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPF-KVT 122  
Db 64 DLTKKSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPFQEK 123  
OY 123 LTGGYLIHYESQLCCQKFLWLPICGAFVYVCIIGCLICLTKKKYSSVHDPNGEYMF 182  
Db 124 LTGGYLIHYESQLCCQKFLWLPICGAFVYVCIIGCLICLTKKKYSSVHDPNGEYMF 183  
OY 183 MRAVNTAKKSRLTDVTL 198  
Db 184 MRAVNTAKKSRLTDVTL 199

RESULT 3

activation-inducible lymphocyte immunostimulatory molecule-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 17-Nov-2000

C:Accession: J07396; PC7099

R:Tezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, Blochem. Biophys. Res. Commun. 276, 335-345, 2000

A:Title: Identification and characterization of rat AILIM/ICOS, a novel T-cell costimulatory molecule

A:Contents: Spleen

A:Accession: J07396

A:Residues: 1-216 <TE2>

A:Accession: PC7099

A:Residues: 21-40 <TE2>

C:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.

A:Gene: a11m-1

C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 64.3%; Score 696; DB 2; Length 216;  
Best Local Similarity 68.8%; Pred. No. 7.3e-60;  
Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2;

OY 7 YF---FLFCLRIKVLTEGINSANVEMFIFHNGVOILCKPDIYQOFKMLKGGQILC 63  
Db 4 YFSCVFVFCFLIKLTGLDLNLRHMFSPHDSGVQISCNPEYQOLKMLFDRVLC 63  
OY 64 DLTKKSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPF-KVT 122  
Db 64 DLTKKSGNTVSIKSLKFCCHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPFQEK 123  
OY 123 LTGGYLIHYESQLCCQKFLWLPICGAFVYVCIIGCLICLTKKKYSSVHDPNGEYMF 182  
Db 124 LTGGYLIHYESQLCCQKFLWLPICGAFVYVCIIGCLICLTKKKYSSVHDPNGEYMF 183  
OY 183 MRAVNTAKKSRL 194  
Db 184 MRAVNTAKKSRL 195

RESULT 4

CD28 precursor - rabbit

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000

C:Accession: S24413; S38722

R:Clark, G.J.; Dallman, M.J.

A:Title: Identification of a cDNA encoding the rat CD28 homologue.

A:Reference number: S24413; MUID:92104640

A:Accession: S24413

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-218 <CLA>

A:Cross-references: EMBL:X55288

R:Clark, G.J.; Dallman, M.J.

submitted to the EMBL Data Library, October 1990

A:Reference number: S38722

A:Accession: S38722

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-152, P, 154-218 <CLA>

A:Cross-references: EMBL:X55288; NID:g55905; PIDN:CAA39003.1; PID:g55906

C:Superfamily: T-cell surface glycoprotein CD28; Immunoglobulin homology

C:Keywords: glycoprotein

F;34-115/Domain: Immunoglobulin homology <IM>

Query Match 14.0%; Score 152; DB 2; Length 218;  
Best Local Similarity 26.2%; Pred. No. 3.1e-07;  
Matches 42; Conservative 25; Mismatches 65; Indels 28; Gaps 7;  
OY 30 MEIRHNGVOILCKYPP--IYQOFKMLKGGQILCDUTKSGNVSISLTK-----F 82  
Db 29 LLYVDNNEVSISCRISNLRKFRASLYK--VNSDEVCGVGNNTYQOFPPNNGFN 86  
OY 83 CHSOLSNNSVSFFLYNLDSHANYFCNLSTFDPPF-KVTLTGVLHYESQLC----- 136  
Db 87 CDGNFDEVTYFLRMNDVNTDIFCKIEYMPPLDNEKSGITIIHKELHCAQT 146  
OY 137 CQLKFLWLPICGAFVYVCIIGC-----ILICWLTKK 168  
Db 147 SPKLFM-----ALVYVAGVILCYGLVTVTLCTITNSRR 181  
RESULT 5  
CD28 precursor - rabbit  
I46689

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OM protein - protein search, using sw model

Run on: July 1, 2002, 16:49:02 ; Search time 11.9 Seconds

(without alignments)  
647,495 Million cell updates/sec

Title: us-09-509-283b-2

Perfect score: 1082

Sequence: 1 MMSGMLYFPLFLIRIVLTG.....YMFRAVNTAKSRITDVTLL 199

## ALIGNMENTS

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	14.7	218	1	CD28_RAT
2	150.5	13.9	221	1	CD28_RABIT
3	141	13.0	219	1	CD28_BOVIN
4	139.5	12.9	220	1	CD28_HUMAN
5	138	12.8	218	1	CD28_MOUSE
6	97	9.0	221	1	CD28_CHICK
7	89	8.2	321	1	OSVI_HUMAN
8	87	8.0	330	1	FCG2_MOUSE
9	86.5	8.0	223	1	CTL4_MOUSE
10	86	7.9	223	1	CTL4_MOUSE
11	82.5	7.6	248	1	VGL2_EBV
12	81	7.5	1382	1	MET_RAT
13	81	7.5	1584	1	YJ9G_YEAST
14	77.5	7.2	324	1	CRFB_SHEEP
15	77.5	7.2	1070	1	PRK7_HUMAN
16	76.5	7.1	223	1	CTL4_RABIT
17	76.5	7.1	323	1	FCG2_HUMAN
18	76	7.0	317	1	FCG2_HUMAN
19	76	7.0	448	1	BCNL_MOUSE
20	76	7.0	450	1	BCNL_MOUSE
21	76	7.0	466	1	ALAD_RABIT
22	76	7.0	562	1	ALAD_MOUSE
23	75.5	7.0	261	1	FCG3_MOUSE
24	75	6.9	462	1	CATC_MOUSE
25	75	6.9	1132	1	VHSI_LAMB
26	74.5	6.9	761	1	AD24_MOUSE
27	74	6.8	344	1	OM40_DROME
28	74	6.8	367	1	ND1M_PODAN
29	73.5	6.8	285	1	FCG2_RAT
30	73.5	6.8	322	1	CRFB_MOUSE
31	73.5	6.8	322	1	CCPH_HSV8
32	73.5	6.8	496	1	GRB_MOUSE
33	73.5	6.8	496	1	GRB_MOUSE

34	73.5	6.8	497	1	GRB_HUMAN	P48167 homo sapien
35	73.5	6.8	1162	1	BXEN_CLOBU	Q06366 clostridium
36	73	6.7	275	1	YD84_YEAST	Q12359 saccharomyc
37	73	6.7	916	1	SCRB_LIMPO	Q25386 limulus pol
38	72.5	6.7	654	1	BFR2_HUMAN	Q01742 homo sapien
39	72	6.7	561	1	ALAD_RAT	P22944 rattus norv
40	72	6.7	569	1	YJ53_YEAST	Q06567 saccharomyc
41	71.5	6.6	634	1	YCX3_EUGER	P31916 euglena gra
42	71.5	6.6	1051	1	PRK7_CHICK	Q91048 gallus gall
43	71	6.6	212	1	KITH_ENCCU	Q96720 encephalito
44	71	6.6	466	1	ALAD_BOVIN	P18130 bos taurus
45	70.5	6.5	524	1	VLI_HPV58	P25535 human papil

RESULT	ID	CD28_RAT	STANDARD:	PRT:	218 AA.
AC	P31042:				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	T-cell-specific surface glycoprotein CD28 precursor.				
GN	CD28.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-DA; TISSUE=Lymphoid;				
RX	MEDLINE=92104640; PubMed=1309509;				
RA	Clark G.J., Dallman M.J.;				
RL	"Identification of a cDNA encoding the rat CD28 homologue";				
RT	Immunogenetics 35:54-57(1992).				
CC	- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1 AND B7-2 (B70).				
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.				
CC	- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.				
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
CC	-----				
DR	EMBL: X55288; CNA39003.1; -.				
DR	PIR: S38722; S38722.				
DR	InterPro: IPR003600; Ig_1-like.				
DR	SMART: SM00410; IG_1like; 1.				
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.				
FT	SIGNAL	1	19		
FT	CHAIN	20	218		
FT					
FT	DOMAIN	20	150		
FT	TRANSMEM	151	177		
FT	DOMAIN	178	218		
FT	DOMAIN	29	138		
FT	CARBOHD	72	72		
FT	CARBOHD	93	93		
FT	CARBOHD	106	106		
FT	CARBOHD	130	130		
SO	SEQUENCE	218 AA;	25170 MM;		

Query Match 14.7%; Score 159; DB 1; Length 218;  
Best local Similarity 26.5%; Pred. No. 2, 1e-08;

Matches	41:	Conservative	30:	Mismatches	66:	Indels	18:	Gaps	7:				
Oy	30	MEIFINGGVOLICKRPD--IYQGFMOQLLGGQILCDLTKTGSGNTYSIKSLK-----F	82										
Db	29	LIVDNNNEVSIISCRSYNLLAKEFASLYKG--VNSDVEVCYGNENFTYQOPFRNVCFN	86										
Oy	83	CHSOLSNNSVFSEFLNLDHSHANYECNLSIEDPPPF--KYVLGTGLHYESQLC---C	137										
Db	87	CDGNFDNEFTVFRMLNDVNNHTDIYFCRKEVYAPPPYLDNENKSNQTIHKKHKLCHNQ	146										
Oy	138	QLKFWLPIGCAAFVYVC--ILGCLILC--WLTKK	168										
Db	147	SPKLEWPLVYVAGVLDLCYGLVTVTLCTIWNSTR	181										
RESULT 2													
ID	CD28_RABIT	STANDARD:	PRT:	221	AA.								
AC	P42069;												
DC	01-NOV-1995 (Rel. 32, Created)												
DE	01-NOV-1995 (Rel. 32, Last sequence update)												
DE	01-MAR-2002 (Rel. 41, Last annotation update)												
GN	T-cell-specific surface glycoprotein CD28 precursor.												
OS	Oryctolagus cuniculus (Rabbit).												
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
OX	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.												
RN	NCBI_taxid:9986;												
RP	[1]												
RT	SEQUENCE FROM N.A.												
RX	STRAIN=B/J X CHB:HM;												
RL	MEDLINE=95369849; PubMed=7642234;												
RA	Isono T., Seta A.;												
RT	"Cloning and sequencing of the rabbit gene encoding T-cell												
RT	costimulatory molecules.";												
RL	Immunogenetics 42:217-220(1995).												
CC	-1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1												
CC	AND B7-2 (B70) (BY SIMILARITY).												
CC	-1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY).												
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.												
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.												
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.												
CC	-----												
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CC	or send an email to <a href="mailto:license@sib-slb.ch">license@sib-slb.ch</a> ).												
CC	-----												
DR	EMBL: D49841; BAA08641.1; "												
DR	InterPro: IPR003600; IG_Like.												

Query Match	13.9%	Score 150.5;	DB 1,	Length 221;
Best Local Similarity	23.8%	Pred. No. 1.4e-07;		
Matches 38;	Conservative 27;	Mismatches 70;	Indels 25;	Gaps 6

```

0y 30 MEIFNNGGQIOLCKPDP--IWOQFMOLKGLQIOLCKTKGKS-----GNVYSIKSL 80
Db 29 MLYVNNNEVNSLCKTYYTLNFSEKFEPAASLYKGDADSAVECYVNGNSHPHQHSTTGFN-- 86
0y 81 KECHSOLSNNSVSEFLYLNLDHSHANYEFCNLSIEDPPEF--KVLTTGGYLIHYESQLC-- 133
Db 87 --CDRLKLGNEYTYELKLNLYNQDTIYCKLEIEMVPPRYLDNEKNSGTLIHVKEQHPCPA 144
0y 137 ----COLKFWLPI---GCAGFVYVVCILGCLIDCWLTKKK 168
Db 145 HPSRKSSTLFWLYLVYGVAVLFAEYSLNLYVALEFSCKMKSKK 184

```

RESULT	3			
CD28_BOVIN				
ID	CD28_BOVIN	STANDARD:	PRT:	219 AA.
AC	Q28071.			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	T-cell-specific surface glycoprotein CD28 precursor.			
GN	CD28.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID:9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:96186531; PubMed=8606060;			
RA	Parsons K.R., Young J.R., Collins R.A., Howard C.J.;			
RT	"Cattle CLA-4, CD28 and chicken CD28 bind CD86: MYPPPY is not			
RL	conserved in cattle CD28 ".			
CC	Immunogenetics 43:388-391(1996).			
CC	- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1			
CC	AND B7-2 (B70).			
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.			
CC	-----			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; X93304; CAA63707.1; -			
DR	InterPro; IPR003600; IG-like.			
DR	SMART; SM00410; IG-like; 1.			
KW	Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.			
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	219	T-CELL-SPECIFIC SURFACE GLYCOPROTEIN
FT				POTENTIAL.
FT				CD28.
FT	DOMAIN	19	151	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	152	178	POTENTIAL.
FT	DOMAIN	179	219	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	28	136	IG-LIKE V-TYPE DOMAIN.
FT	CARBOHD	37	37	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	71	71	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	84	84	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	91	91	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	104	104	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHD	128	128	N-LINKED (GLCNAc. . .) (POTENTIAL).
SO	SEQUENCE	219 AA;	25143 MW;	85B5C650D96534AA CRC64;

Query Match	13.0%;	Score 141;	DB 1;	Length 219;
Best Local Similarity	23.2%;	Pred. No. 1.2e-06;		
Matches	36;	Conservative	32;	Mismatches 71;
			Indels	16;
			Gaps	6;



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OM protein - protein search, using sw model

Run on: July 1, 2002, 16:48:37 ; Search time 26.62 Seconds

(without alignments)  
1293.238 Million cell updates/sec

Title: US-09-509-283b-2

Perfect score: 1082  
Sequence: 1 MMSGIMWFYFLCLRIKIVLTG.....YMFMAVNTAKKSRLTDVTL 199

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082	100.0	199	4	Q9Y6W8
2	737.5	68.2	200	11	Q9WVS0
3	734	67.8	200	11	Q9JIL7
4	701	64.8	200	11	Q9RI77
5	696	64.3	216	11	Q9WVR9
6	146.5	13.5	221	11	Q9JLV4
7	145.5	13.4	221	6	Q9N2I4
8	145.5	13.4	221	6	002757
9	145	13.0	219	6	Q97630
10	140.5	13.0	221	6	Q9GKP3
11	139.5	12.9	221	6	Q9N0N8
12	139.5	12.6	173	6	Q28289
13	136.5	12.5	220	6	Q9BDM8
14	135.5	12.1	220	6	Q9BDM5
15	130.5	11.6	220	6	Q9BDM6
16	125.5	11.6	220	6	Q9BDN8

17	115.5	10.7	220	6	Q9BDN2	Q9bdn2 callithrix
18	103.5	9.6	988	5	Q17710	Q17710 caenorhabdi
19	91.5	8.5	485	5	Q20139	Q20139 caenorhabdi
20	87	8.0	223	6	Q9BDP1	Q9bdp1 actus trivi
21	84.5	7.8	209	4	Q9NYK4	Q9nyk4 homo sapien
22	84.5	7.8	223	11	Q9QZ27	Q9qz27 mus musculu
23	84	7.8	223	4	Q96P43	Q96p43 homo sapien
24	84	7.8	285	17	Q28747	Q28747 archaeoglob
25	84	7.8	419	13	Q9IA91	Q9ia91 morone saxa
26	83.5	7.7	223	11	Q9JLV3	Q9jlv3 marmota mon
27	83	7.7	1239	10	Q9FHM1	Q9fhm1 araldopsis
28	82.5	7.6	223	11	Q62859	Q62859 rattus norv
29	82	7.6	223	6	Q9BDC4	Q9bdc4 macaca mula
30	82	7.6	223	6	Q9BDN7	Q9bdn7 papio anubi
31	81	7.5	276	12	Q98822	Q98822 human adeno
32	81	7.5	276	12	Q64861	Q64861 human adeno
33	81	7.5	680	11	Q55001	Q55001 mus musculu
34	80.5	7.4	247	16	Q99RX6	Q99rx6 staphylococ
35	80.5	7.4	635	11	Q55002	Q55002 mus musculu
36	80.5	7.4	663	11	Q70434	Q70434 mus musculu
37	79.5	7.3	269	4	Q95297	Q95297 homo sapien
38	79	7.3	370	4	Q9BZM8	Q9bzm8 homo sapien
39	78.5	7.3	310	11	Q9EQ87	Q9eq87 mus musculu
40	78	7.2	231	5	Q45668	Q45668 caenorhabdi
41	77.5	7.2	311	11	Q9EQ86	Q9eq86 mus musculu
42	77	7.1	323	6	Q9BDM2	Q9bdm2 cercopithec
43	77	7.1	338	5	Q22576	Q22576 caenorhabdi
44	77	7.1	539	12	P88842	P88842 avian infec
45	77	7.1	619	10	Q9XGJ1	Q9xgj1 sorghum b1c

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	199 AA.
Q9Y6W8	09Y6W8			
AC	Q9Y6W8			
DT	01-NOV-1999 (TREMBLrel. 12, Created)			
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE AILIM			
DE	PRECURSOR (INDUCIBLE T-CELL CO-STIMULATOR PRECURSOR) (INDUCIBLE			
DE	COSTIMULATOR PRECURSOR).			
GN	ICOS.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN				
RP	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE-BLOOD;			
RA	Tezuka K., Tamatani T.;			
RT	"Cell surface molecule mediating cell adhesion and signal			
RL	transmission";			
RL	submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99127892; PubMed=9930702;			
RA	Hutloff A., Dittlich A.M., Beier K.C., Eljaschewitsch B., Kraft R.,			
RT	Aganostopoulos I., Krocsek R.A.;			
RL	ICOS is an inducible T-cell co-stimulator structurally and			
RT	functionally related to CD28.;"			
RL	Nature 397:263-266(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Beier K.C., Hutloff A., Dittlich A.M., Heuck C., Mages H.W.,			
RT	Buecher K., Henn V., Rauch A., Krocsek R.A.;			
RL	"Detailed analysis of human ICOS and its ligand.;"			
RT	submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=THYMUS;			

RA MEDLINE=20243570;  
 RA Aicher A., Hayden-Ledbetter M., Brady W.A., Pezzutto A., Richter G.,  
 RA Magerle D., Buckwalter S., Ledbetter J.A., Clark E.A.;  
 RT "Characterization of human inducible costimulator ligand expression  
 RT and function.";  
 RL J. Immunol. 164:4689-4696(2000).  
 DR EMBL: AB023135; BA082129.1; -;  
 DR EMBL: AJ277832; CAC06512.1; -;  
 DR EMBL: AF218312; AAF71301.1; -;  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 199 AA; 22624 MM; 214EC741C9BDC9FC CRC64;

Query Match 100.0%; Score 1082; DB 4; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 2, 8e-109;  
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSLWFFELFCLRIKIVLTGEINGSANYEMFIHNGVQILCKYPDIVQCFKMLKGGQ 60  
 1 MKSLWFFELFCLRIKIVLTGEINGSANYEMFIHNGVQILCKYPDIVQCFKMLKGGQ 60  
 QY 61 ILCLTKGSGNVTSTKSLKFSQSLSNSVSFEVLNLDHSHANYFCNLTIFDPPPEK 120  
 61 ILCLTKGSGNVTSTKSLKFSQSLSNSVSFEVLNLDHSHANYFCNLTIFDPPPEK 120  
 Db 61 ILCLTKGSGNVTSTKSLKFSQSLSNSVSFEVLNLDHSHANYFCNLTIFDPPPEK 120  
 QY 121 VTLGGYLHYESQLCCQLKFWLPICGAFVVCILGICILTLTKKRYSSVHPDNGEX 180  
 121 VTLGGYLHYESQLCCQLKFWLPICGAFVVCILGICILTLTKKRYSSVHPDNGEX 180  
 Db 121 VTLGGYLHYESQLCCQLKFWLPICGAFVVCILGICILTLTKKRYSSVHPDNGEX 180  
 QY 181 MFMAVNTAKSRRLDVT 199  
 181 MFMAVNTAKSRRLDVT 199  
 Db 181 MFMAVNTAKSRRLDVT 199

RESULT 2  
 Q9WVS0 PRELIMINARY; PRT; 200 AA.

AC Q9WVS0;  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMODULATOR MOLECULE ALLIM  
 DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).  
 GN CCIP OR ICOS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Tezuka K., Tametani T.;  
 RT "Cell surface molecule mediating cell adhesion and signal  
 RT transmission.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=SPLEEN;  
 RA Wu D., Glanville M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,  
 RA Matis L.A., Rother R.P.;  
 RT "CCIP, A novel molecule that regulates T cell activation.";  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=SPLEEN;  
 RX MEDLINE=20225659; PubMed=10760791;  
 RA Mages H.W., Hutloff A., Heuck C., Buchner K., Himmelfauer H.,  
 RA Clivieri F., Kiocek R.A.;  
 RT "Molecular cloning and characterization of murine ICOS and  
 RT identification of B7h as ICOS ligand.";  
 RL Eur. J. Immunol. 30:1040-1047(2000).  
 DR EMBL: AB023132; BA082126.1; -;

DR EMBL: AF257230; AAF70099.1; -;  
 DR EMBL: AJ250559; CAB71153.1; -;  
 DR MGD; MGI:1858745; Icos.  
 KW Signal.  
 FT SIGNAL.  
 SQ SEQUENCE 1 20 POTENTIAL.  
 9B2278EACABIDB47 CRC64;

Query Match 68.2%; Score 737.5; DB 11; Length 200;  
 Best Local Similarity 69.3%; Pred. No. 6e-72;  
 Matches 138; Conservative 20; Mismatches 40; Indels 1; Gaps 1;

QY 1 MKSLWFFELFCLRIKIVLTGEINGSANYEMFIHNGVQILCKYPDIVQCFKMLKGGQ 60  
 1 MKSLWFFELFCLRIKIVLTGEINGSADHRMFSFHNGVQILCKYPDIVQCFKMLRFRERE 60  
 Db 1 MKPYCHVFVFCPLRIKIVLTGEINGSADHRMFSFHNGVQILCKYPDIVQCFKMLRFRERE 60  
 QY 61 ILCLTKGSGNVTSTKSLKFSQSLSNSVSFEVLNLDHSHANYFCNLTIFDPPPEK 120  
 61 ILCLTKGSGNVTSTKSLKFSQSLSNSVSFEVLNLDHSHANYFCNLTIFDPPPEK 120  
 Db 61 ILCLTKGSGNVTSTKSLKFSQSLSNSVSFEVLNLDHSHANYFCNLTIFDPPPEK 120  
 QY 121 VTLGGYLHYESQLCCQLKFWLPICGAFVVCILGICILTLTKKRYSSVHPDNGEX 179  
 121 VTLGGYLHYESQLCCQLKFWLPICGAFVVCILGICILTLTKKRYSSVHPDNGEX 179  
 Db 121 VTLGGYLHYESQLCCQLKFWLPICGAFVVCILGICILTLTKKRYSSVHPDNGEX 180  
 QY 180 YMFMAVNTAKSRRLDVT 198  
 180 YMFMAVNTAKSRRLDVT 198  
 Db 180 YMFMAVNTAKSRRLDVT 198

RESULT 3  
 Q9JL17 PRELIMINARY; PRT; 200 AA.

AC Q9JL17;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE CD28-RELATED PROTEIN 1 (INDUCIBLE COSTIMULATOR PROTEIN)  
 DE (FRAGMENT).  
 GN ICOS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=INTESPRINAL; INTRA-EPITHELIUM;  
 RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,  
 RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafurt-Bladt A.,  
 RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,  
 RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,  
 RA Senaldi G.;  
 RT "T-cell co-stimulation through B7RP-1 and ICOS.";  
 RL Nature 0:0-0(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Ola;  
 RA McAdam A.J., Greenwald R.J., Levin M.A., Chernova T., Malenkovich N.,  
 RA Ling V., Freeman G.J., Sharpe A.H.;  
 RT "The inducible costimulator (ICOS) molecule is critical for CD40-  
 RT mediated antibody class switching.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF216748; AAF45150.1; -;  
 DR EMBL: AF327185; AAG48732.1; -;  
 DR EMBL: AF327184; AAG48732.1; JOINED.  
 FT NON TER 200  
 SQ SEQUENCE 200 AA; 22709 MM; 87D97F0DC44ADC47 CRC64;

Query Match 67.8%; Score 734; DB 11; Length 200;  
 Best Local Similarity 70.4%; Pred. No. 1.4e-71;  
 Matches 138; Conservative 19; Mismatches 35; Indels 4; Gaps 2;  
 QY 7 YF---FLFCLRIKIVLTGEINGSANYEMFIHNGVQILCKYPDIVQCFKMLKGGQILC 63

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Db      4 YFCRFVCFECFLIRLLTGLTEINGSADHRMFSGFHNGGVQISCKYDETVQQLAMRLFREVEVLG 63
Oy      64 DLTTRKSGSNWYSIKSLKFCCHSOLSNNSVSFFLYNLIDHSHANYPCNLSIFPPPPPKV-T 122
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      64 ELTKRKSGSNAVSINPNMCLYLHLSNNSVSFFELNPDDSSOGSYFCSLSIFPPPPPEQRN 123
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Oy      123 LTGGYLHIYESQLCCQLKFWMLPICGAAPVVCVILGCILLCMETLTKKKYSSVDHPDNEYNWF 182
        |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      124 LSGYLHIYESQLCCQLKTMLPVGCAAFVVALFGCILLIMFSKKKYSSVDHPDNEYNWF 183
Oy      183 MRAVNTAKKSRLTDVT 198
        |::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      184 MAAVNTNKKSRLAGVT 199

RESULT 4
O9RIT7 PRELIMINARY; PRT; 200 AA.
ID O9RIT7
AC O9RIT7;
NC_01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
PRECURSOR.
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
OR RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20462959; PubMed=11006126;
RA Tezuka K., Tsuji T., Hirano D., Yamatani T., Sakamaki K.,
RA Kobayashi Y., Kanada M.;
RT "Identification and characterization of rat Ailim/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL: AB023134; BAA82128.1; -.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 200 AA; 22529 MW; 0A4C3581E129D4 CRC64;

Query Match 64.8%; Score 701; DB 11; Length 200;
Best Local Similarity 67.9%; Pred. No. 5.4e-68;
Matches 133; Conservative 17; Mismatches 42; Indels 4; Gaps 2
Oy      7 YF--FLECLRIRKIVLTGEINGSANTEMFIHFHGVOIICKRYDVOOFKMOLKGQILC 63
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
        4 YFSCVFVFCFLIKTLTGELDLNLRHMFSGFHNGGVQISCNYPETVQQLKMQLFKDREVLC 63
Oy      64 DLTTRKSGSNWYSIKSLKFCCHSOLSNNSVSFFLYNLIDHSHANYPCNLSIFPPPP-KYT 122
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      64 DLTTRKSGSNWYSIKSNPMSCPYQLSNSVSFFELNDASDSQSIFCLSLIFPPPPPEQRN 123
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Oy      123 LTGGYLHIYESQLCCQLKFWMLPICGAAPVVCVILGCILLCMETLTKKKYSSVDHPDNEYNWF 182
        |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      124 LSGYLHIYESQLCCQLKTMLPVGCAAFVVALFGCILLIMFSKKKYSSVDHPDNEYNWF 183
Oy      183 MRAVNTAKKSRLTDVT 198
        |::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      184 MAAVNTNKKSRLAGMT 199

RESULT 5
O9WVR9 PRELIMINARY; PRT; 216 AA.
ID O9WVR9
AC O9WVR9;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
PRECURSOR.
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OC Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA MEDLINE=20462959; PubMed=11066126;
RX Tezuka K., Tsuji T., Hirano D., Tametani T., Sakamaki K.,
RA Kobayashi Y., Kamada M.;
RT "Identification and characterization of rat ALLIM/ICOS, a novel T-cell
RT costimulatory molecule, related to the CD28/CTLA4 family.";
RL Biochem. Biophys. Res. Commun. 276:335-345(2000).
DR EMBL; AB023133; BAA82127.1; -.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 216 AA; 24260 MW; 772E01320982B15A CRC64;
    POTENTIAL.

Query Match          64.3%; Score 696; DB 11; Length 216;
Best Local Similarity 68.8%; Pred. No. 2.1e-67;
Matches 132; Conservative 16; Mismatches 40; Indels 4; Gaps 2

OY YE---FICLCIRKIVLTGETINGSANTEMFFHNGVGQIICKYDYOQFMOLLKGQIIIC 63
Db |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 63
   4 YFSCVFEVCELIKTLTGETINDIANRHSEFHGCGVQISCNVEFYQOLMKLFKDREVL 63
OY 64 DLTKRGSGNTYSIKSLKFCHSOLSNSNVSFFLYNLDSHAVYFCNLSIFDPPEP-KYT 122
Db 64 DLTRKGSNGNTYSINPNMSCPRLOSNVSFFLDNADNSQSGLFCLSDIFDPPEQEK 123
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 123
OY 123 LTGGLVHIYESQLCQQLKFWLPICGAAPVVCILGCILICWLTKKRYSSVDHPGEYMF 182
Db 124 LSGGLLLYYESQLCQQLKLMPGVCAAFVAALLFGCIFLWPAKKRRYSVDHPNSEYMF 183
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 183
OY 183 MRAVNTAKKSRL 194
Db 184 MAAVNTNKKSRL 195
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 195

RESULT 6
ID O9JLV4 PRELIMINARY; PRT; 221 AA.
AC O9JLV4
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CD28 ANTIGEN.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Sciuridae; Scurinae;
OC Marmota.
CX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu M., Yang D., Kemper T., Maier A., Roggendorf M.;
RT "Molecular characterization of woodchuck CD28 and cytotoxic T-
RT lymphocyte associated antigen 4 (CTLA-4).";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL; AF104247; AAF6501.1; -.
DR InterPro: IPR003600; IG_1like.
DR SMART: SM00410; IG_1like; 1.
SQ SEQUENCE 221 AA; 25594 MW; B29D32E987CE51D1 CRC64;

Query Match          13.5%; Score 146.5; DB 11; Length 221;
Best Local Similarity 23.0%; Pred. No. 7.6e-08;
Matches 43; Conservative 36; Mismatches 71; Indels 37; Gaps 7

OY 14 RIKVLTGETINGSANTEMFFHNGVGQIICKYDYOQFMOLLKGQIICDLTKRGSGN 73
Db |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::| 73
   29 RLEVYNNEENLSCKTYTNLEF-----KEFRASYLKGVDSAIVECYVANGNS 74

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QY 74 TVSIKSLKF-----CHSOLSNNSVSEFLYNLDHSHANYFCNLSTFDPPPF--KVTLT 124  
ID 09N214 PRELIMINARY; PRT; 221 AA.  
AC 09N214  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2001 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
CD28.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:20094001; PubMed:10630305;  
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,  
RA Mikami T., Takahashi E.;  
RT "Molecular cloning and sequencing of a cDNA encoding the feline T-cell  
RT antigen CD28 homologue."  
RL Immunogenetics 50:369-370(1999).  
DR EMBL: AB025316; BAA92349.1; -.  
DR InterPro: IPR003600; Ig\_Like.  
DR SMART: SM00410; Ig\_Like.1.  
SQ SEQUENCE 221 AA; 25283 MW; B17B76C52BA18DCB CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;  
Best Local Similarity 28.3%; Pred. No. 9.8e-08;  
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGVOILCKYPD--IVQFKMQLKGGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
ID 002757 PRELIMINARY; PRT; 221 AA.  
AC 002757;  
DT 01-JUL-1997 (Tremblrel. 04, Created)  
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Hash S.M., Carpino M.R., Collisson E.W.;  
RA "Feline catus T-cell specific surface glycoprotein CD28."  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

QY 125 GGYHITESQLCCOL-----KFM-LPIGCAAFVVCILCICILCWLTKKYSVVDP 176  
ID 131 GTVIHVENNICPGSPVSPPEPKPFMTLVFSGVLGIYSTLMILCYLMTKRRTRL--L 188  
DT 177 NGEMFM 183  
DB 189 QSDYMM 195

RESULT 7  
ID 09N214 PRELIMINARY; PRT; 221 AA.  
AC 09N214  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2001 (Tremblrel. 15, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
CD28.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:20094001; PubMed:10630305;  
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,  
RA Mikami T., Takahashi E.;  
RT "Molecular cloning and sequencing of a cDNA encoding the feline T-cell  
RT antigen CD28 homologue."  
RL Immunogenetics 50:369-370(1999).  
DR EMBL: AB025316; BAA92349.1; -.  
DR InterPro: IPR003600; Ig\_Like.  
DR SMART: SM00410; Ig\_Like.1.  
SQ SEQUENCE 221 AA; 25283 MW; B17B76C52BA18DCB CRC64;

RL Thesis (1996), Veterinary Pathobiology, Texas A&M Univ.  
DR EMBL: U57754; AAB53574.1; -.  
DR InterPro: IPR003600; Ig\_Like.  
DR SMART: SM00410; Ig\_Like.1.  
SQ SEQUENCE 221 AA; 25317 MW; 5B71717E461AE5E3 CRC64;

Query Match 13.4%; Score 145.5; DB 6; Length 221;  
Best Local Similarity 28.3%; Pred. No. 9.8e-08;  
Matches 45; Conservative 22; Mismatches 65; Indels 27; Gaps 8;

QY 32 IFHNGVOILCKYPD--IVQFKMQLKGGQILCDLTKTKG--SGNTVSIKSLKF-CHSQ 86  
ID 097630 PRELIMINARY; PRT; 219 AA.  
AC 097630;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE T-CELL SPECIFIC SURFACE GLYCOPROTEIN CD28.  
GN CD28.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE:99309828; PubMed:10380709;  
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;  
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4."  
RL Immunogenetics 49:583-584(1999).  
DR EMBL: AF092739; AAD04379.1; -.  
DR InterPro: IPR003600; Ig\_Like.  
DR SMART: SM00410; Ig\_Like.1.  
SQ SEQUENCE 219 AA; 25158 MW; D50AD339E5BC2327 CRC64;

Query Match 13.4%; Score 145; DB 6; Length 219;  
Best Local Similarity 23.5%; Pred. No. 1.1e-07;  
Matches 40; Conservative 35; Mismatches 75; Indels 20; Gaps 8;

QY 30 MFITHNGVOILCKYPD--IVQFKMQLKGGQILCDLTKTKG--GNTVSIKSLKF-CHS 85  
ID 28 MLVNDNEVNLSCRYTNLFESKEFRASLYKGADSAVECAVNGNHSHPLOSTNKEFNCTV 87  
DB 86 QLSNNSVSEFLYNLDHSHANYFCNLSTFDPPPF--KVTLTGGYLIHYESQLC----- 136  
DT 88 KVGNETYVFIQDLVYNQTDYIFCKLEVLPYPPYIDNEKSNGTITIHVEKHLCPAQLSPES 147  
QY 137 QQLKFWLPI---GCAAFVVCILCICILCWLTKKYSVVDPNGEYMF 183  
ID 148 SSKFMAVLVYVNGLVFYSLLVVALCNCWKKSR--NRMH--QSDYMM 193  
DB 148 SSKFMAVLVYVNGLVFYSLLVVALCNCWKKSR--NRMH--QSDYMM 193

RESULT 10  
ID 09GKP3 PRELIMINARY; PRT; 221 AA.  
AC 09GKP3;  
DT 01-MAR-2001 (Tremblrel. 16, Created)  
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 1, 2002, 16:47:37 ; Search time 13.12 Seconds

(without alignments)  
370,480 Million cell updates/sec

Title: US-09-509-283B-2

Perfect score: 1082

Sequence: 1 MMSGIMWFPLFCIRIVLTG.....YMFRAVNTAKSRLDVTLL 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCITUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	15.1	218	3	US-08-228-208A-20
2	146.5	13.5	225	1	US-08-505-058-4
3	146.5	13.5	225	2	US-08-459-818-24
4	146.5	13.5	225	2	US-08-889-666-24
5	146.5	13.5	225	2	US-08-465-078-24
6	146.5	13.5	225	2	US-08-725-776-24
7	146.5	13.5	225	2	US-08-488-062-24
8	140	12.9	218	3	US-08-228-208A-19
9	134.5	12.4	220	3	US-08-228-208A-21
10	134	12.4	225	1	US-08-505-058-3
11	134	12.4	225	2	US-08-459-818-23
12	134	12.4	225	2	US-08-889-666-23
13	134	12.4	225	2	US-08-465-078-23
14	134	12.4	225	2	US-08-725-776-23
15	134	12.4	225	2	US-08-488-062-23
16	126	11.6	223	1	US-08-505-058-5
17	126	11.6	223	2	US-08-459-818-25
18	126	11.6	223	2	US-08-889-666-25
19	126	11.6	223	2	US-08-465-078-25
20	126	11.6	223	2	US-08-725-776-25
21	126	11.6	223	2	US-08-488-062-25
22	120.5	11.1	367	3	US-08-630-172-19
23	120.5	11.1	367	4	US-09-375-419-19
24	119.5	11.0	134	3	US-08-630-172-3
25	119.5	11.0	134	4	US-09-375-419-3
26	110.5	10.2	110	4	US-09-460-384-33
27	93	8.6	221	3	US-08-228-208A-22

28	89.5	8.3	117	2	US-08-529-878B-39	Sequence 39, Appl
29	87	8.0	330	2	US-08-332-562A-81	Sequence 81, Appl
30	87	8.0	330	2	US-08-332-562A-134	Sequence 134, Appl
31	86.5	8.0	209	4	US-09-430-503-20	Sequence 20, Appl
32	86.5	7.8	209	4	US-09-430-503-18	Sequence 18, Appl
33	84.5	7.8	209	4	US-09-430-503-24	Sequence 24, Appl
34	84	7.8	223	3	US-08-228-208A-17	Sequence 17, Appl
35	84	7.8	283	3	US-08-332-562A-136	Sequence 136, Appl
36	82.5	7.6	209	4	US-09-430-503-22	Sequence 22, Appl
37	81.5	7.5	187	1	US-08-067-684-14	Sequence 14, Appl
38	81.5	7.5	187	1	US-08-008-898-14	Sequence 14, Appl
39	81.5	7.5	187	2	US-08-459-818-14	Sequence 14, Appl
40	81.5	7.5	187	2	US-08-889-666-14	Sequence 14, Appl
41	81.5	7.5	187	2	US-08-465-078-14	Sequence 14, Appl
42	81.5	7.5	187	2	US-08-725-776-14	Sequence 14, Appl
43	81.5	7.5	187	2	US-08-488-062-14	Sequence 14, Appl
44	81.5	7.5	187	3	US-08-228-208A-14	Sequence 14, Appl
45	81.5	7.5	187	5	PCT-US95-06726-36	Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
US-08-228-208A-20  
Sequence 20, Application US/08228208A  
Patent No. 6090914  
GENERAL INFORMATION:  
APPLICANT: Linsley, Peter S.  
APPLICANT: Ledbetter, Jeffrey A.  
APPLICANT: Dame, Nita K.  
APPLICANT: Brady, William  
APPLICANT: Wallace, Philip M.  
TITLE OF INVENTION: CTLA4/CD28 HYBRID FUSION  
TITLE OF INVENTION: PROTEINS AND USES THEREOF  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Merchant & Gould  
STREET: 1150 Santa Monica Boulevard, Suite 400  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/228, 208A  
FILING DATE: 15-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008, 898  
FILING DATE: 22-JAN-1993  
APPLICATION NUMBER: 07/723, 617  
FILING DATE: 27-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436-30US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310 445-1140  
TELEFAX: 310 445-9031  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-228-208A-20

